



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/085,233 A  
Source: OIPE  
Date Processed by STIC: 6/17/02

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
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<http://www.uspto.gov/web/offices/pac/checker>

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
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2011 South Clark Place, Arlington, VA 22202
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Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202



OIPE

Does Not Comply  
Corrected Diskette Needed See pg. 7

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/085,233A

DATE: 06/17/2002

TIME: 14:46:04

for explanation of  
errors

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\06172002\J085233A.raw

3 <110> APPLICANT: YISSUM Research Development Company of the Hewbrew University of Jerusalem

5 <120> TITLE OF INVENTION: Fce-PE CHIMERIC PROTEIN FOR TARGETED TREATMENT OF ALLERGY RESPONSES, A

6 METHOD FOR ITS PRODUCTION AND PHARMACEUTICAL COMPOSITIONS CONTAINING THE SAME

8 <130> FILE REFERENCE: 1268-067

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/085,233A

C--> 11 <141> CURRENT FILING DATE: 2002-06-10

13 <150> PRIOR APPLICATION NUMBER: IL 116436

14 <151> PRIOR FILING DATE: 1995-12-18

16 <150> PRIOR APPLICATION NUMBER: PCT / IL96 / 00181

17 <151> PRIOR FILING DATE: 1996-12-18

19 <160> NUMBER OF SEQ ID NOS: 8

21 <170> SOFTWARE: PatentIn version 3.0

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 1512

25 <212> TYPE: DNA

C--> 26 <213> ORGANISM: Artificial

28 <220> FEATURE:

29 <223> OTHER INFORMATION: Description of Artificial Sequence: Fce2-3-PE40

31 <220> FEATURE:

32 <221> NAME/KEY: CDS

33 <222> LOCATION: (1)..(1512)

35 <400> SEQUENCE: 1

36 atg gag cag caa tgg atg tct gaa agc acc ttc acc tgc aag gtc acc 48

37 Met Glu Gln Gln Trp Met Ser Glu Ser Thr Phe Thr Cys Lys Val Thr

38 1 5 10 15

40 tcc caa ggc gta gac tat ttg gcc cac act cgg aga tgc cca gat cat 96

41 Ser Gln Gly Val Asp Tyr Leu Ala His Thr Arg Arg Cys Pro Asp His

42 20 25 30

44 gag cca gcc ggt gtg att acc tac ctg atc cca ccc agc ccc ctg gac 144

45 Glu Pro Ala Gly Val Ile Thr Tyr Leu Ile Pro Pro Ser Pro Leu Asp

46 35 40 45

48 ctg tat caa aac ggt gct ccc aag ctt acc tgt ctg gtg gtg gac ctg 192

49 Leu Tyr Gln Asn Gly Ala Pro Lys Leu Thr Cys Leu Val Val Asp Leu

50 50 55 60

52 gaa agc gag aag aat gtc aat gtg acg tgg aac caa gag aag aag act 240

53 Glu Ser Glu Lys Asn Val Asn Val Thr Trp Asn Gln Glu Lys Lys Thr

54 65 70 75 80

56 tca gtc tca gca tcc cag tgg tac act aag cac cac aat aac gcc aca 288

57 Ser Val Ser Ala Ser Gln Trp Tyr Thr Lys His His Asn Asn Ala Thr

58 85 90 95

60 act agt atc acc tcc atc ctg cct gta gtt gcc aag gac tgg att gaa 336

61 Thr Ser Ile Thr Ser Ile Leu Pro Val Val Ala Lys Asp Trp Ile Glu

62

100

105

110

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Input Set : A:\pto.vsk.txt

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64 ggc tac ggc tat cag tgc ata gtg gac cac cct gat ttt ccc aag ccc      384
65 Gly Tyr Gly Tyr Gln Cys Ile Val Asp His Pro Asp Phe Pro Lys Pro
66      115      120      125
68 att gtg cgt tcc atc acc aag acc cca cat atg gcc gaa gag ggc ggc      432
69 Ile Val Arg Ser Ile Thr Lys Thr Pro His Met Ala Glu Glu Gly Gly
70      130      135      140
72 agc ctg gcc gcg ctg acc gcg cac cag gct tgc cac ctg ccg ctg gag      480
73 Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu
74 145      150      155      160
76 act ttc acc cgt cat cgc cag ccg cgc ggc tgg gaa caa ctg gag cag      528
77 Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln
78      165      170      175
80 tgc ggc tat ccg gtg cag ccg ctg gtc gcc ctc tac ctg gcg gcg ccg      576
81 Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg
82      180      185      190
84 ctg tcg tgg aac cag gtc gac cag gtg atc cgc aac gcc ctg gcc agc      624
85 Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser
86      195      200      205
88 ccc gcc agc gcc gcc gac ctg gcc gaa gcg atc cgc gag cag ccg gag      672
89 Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu
90      210      215      220
92 cag gcc cgt ctg gcc ctg acc ctg gcc gcc gcc gag agc gag cgc ttc      720
93 Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe
94 225      230      235      240
96 gtc cgg cag gcc acc gcc aac gac gag gcc gcc gcc aac gcc gac      768
97 Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp
98      245      250      255
100 gtg gtg agc ctg acc tgc ccg gtc gcc gcc ggt gaa tgc gcg gcc ccg      816
101 Val Val Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro
102      260      265      270
104 gcg gac agc gcc gac gcc ctg ctg gag cgc aac tat ccc act gcc gcg      864
105 Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala
106      275      280      285
108 gag ttc ctc gcc gac gcc gcc gac gtc agc ttc agc acc cgc gcc acg      912
109 Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr
110      290      295      300
112 cag aac tgg acg gtg gag cgg ctg ctc cag gcg cac cgc caa ctg gag      960
113 Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu
114 305      310      315      320
116 gag cgc gcc tat gtg ttc gtc gcc tac cac gcc acc ttc ctc gaa gcg      1008
117 Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala
118      325      330      335
120 gcg caa agc atc gtc ttc gcc ggg gtg cgc gcg cgc agc cag gac ctc      1056
121 Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu
122      340      345      350
124 gac gcg atc tgg cgc ggt ttc tat atc gcc gcc gat ccg gcg ctg gcc      1104
125 Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala
126      355      360      365
128 tac gcc tac gcc cag gac cag gaa ccc gac gca cgc gcc cgg atc cgc      1152

```

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Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\06172002\J085233A.raw

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129 Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg
130      370      375      380
132 aac ggt gcc ctg ctg cgg gtc tat gtc ccg cgc tcg agc ctg ccg ggc      1200
133 Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly
134 385      390      395      400
136 ttc tac cgc acc agc ctg acc ctg gcc gcg ccg gag gcg gcg ggc gag      1248
137 Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu
138      405      410      415
140 gtc gaa cgg ctg atc ggc cat ccg ctg ccg ctg cgc ctg gac gcc atc      1296
141 Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile
142      420      425      430
144 acc ggc ccc gag gag gaa ggc ggg cgc ctg gag acc att ctc ggc tgg      1344
145 Thr Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp
146      435      440      445
148 ccg ctg gcc gag cgc acc gtg gtg att ccc tcg gcg atc ccc acc gac      1392
149 Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp
150      450      455      460
152 ccg cgc aac gtc ggc ggc gac ctc gac ccg tcc agc atc ccc gac aag      1440
153 Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys
154 465      470      475      480
156 gaa cag gcg atc agc gcc ctg ccg gac tac gcc agc cag ccc ggc aaa      1488
157 Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys
158      485      490      495
160 ccg ccg cgc gag gac ctg aag taa      1512
161 Pro Pro Arg Glu Asp Leu Lys
162      500
165 <210> SEQ ID NO: 2
166 <211> LENGTH: 503
167 <212> TYPE: PRT
C--> 168 <213> ORGANISM: Artificial
W--> 170 <220> FEATURE:
W--> 170 <223> OTHER INFORMATION:
170 <400> SEQUENCE: 2
172 Met Glu Gln Gln Trp Met Ser Glu Ser Thr Phe Thr Cys Lys Val Thr
173 1      5      10      15
176 Ser Gln Gly Val Asp Tyr Leu Ala His Thr Arg Arg Cys Pro Asp His
177      20      25      30
180 Glu Pro Ala Gly Val Ile Thr Tyr Leu Ile Pro Pro Ser Pro Leu Asp
181      35      40      45
184 Leu Tyr Gln Asn Gly Ala Pro Lys Leu Thr Cys Leu Val Val Asp Leu
185      50      55      60
188 Glu Ser Glu Lys Asn Val Asn Val Thr Trp Asn Gln Glu Lys Lys Thr
189 65      70      75      80
192 Ser Val Ser Ala Ser Gln Trp Tyr Thr Lys His His Asn Asn Ala Thr
193      85      90      95
196 Thr Ser Ile Thr Ser Ile Leu Pro Val Val Ala Lys Asp Trp Ile Glu
197      100      105      110
200 Gly Tyr Gly Tyr Gln Cys Ile Val Asp His Pro Asp Phe Pro Lys Pro
201      115      120      125

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DATE: 06/17/2002

PATENT APPLICATION: US/10/085,233A

TIME: 14:46:04

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\06172002\J085233A.raw

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204 Ile Val Arg Ser Ile Thr Lys Thr Pro His Met Ala Glu Glu Gly Gly
205      130      135      140
208 Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu
209 145      150      155      160
212 Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln
213      165      170      175
216 Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg
217      180      185      190
220 Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser
221      195      200      205
224 Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu
225      210      215      220
228 Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe
229 225      230      235      240
232 Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp
233      245      250      255
236 Val Val Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro
237      260      265      270
240 Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala
241      275      280      285
244 Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr
245      290      295      300
248 Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu
249 305      310      315      320
252 Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala
253      325      330      335
256 Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu
257      340      345      350
260 Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala
261      355      360      365
264 Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg
265      370      375      380
268 Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly
269 385      390      395      400
272 Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu
273      405      410      415
276 Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile
277      420      425      430
280 Thr Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp
281      435      440      445
284 Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp
285      450      455      460
288 Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys
289 465      470      475      480
292 Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys
293      485      490      495
296 Pro Pro Arg Glu Asp Leu Lys
297      500
300 <210> SEQ ID NO: 3

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## RAW SEQUENCE LISTING

DATE: 06/17/2002

PATENT APPLICATION: US/10/085,233A

TIME: 14:46:04

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\06172002\J085233A.raw

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301 <211> LENGTH: 2031
302 <212> TYPE: DNA
C--> 303 <213> ORGANISM: Artificial
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Description of Artificial Sequence: Fce2-4-PE40
308 <220> FEATURE:
309 <221> NAME/KEY: CDS
310 <222> LOCATION: (1)..(2031)
312 <400> SEQUENCE: 3
313 atg cga cct gtc aac atc act gag ccc acc ttg gag cta ctc cat tca      48
314 Met Arg Pro Val Asn Ile Thr Glu Pro Thr Leu Glu Leu Leu His Ser
315 1          5          10          15
317 tcc tgc gac ccc aat gca ttc cac tcc acc atc cag ctg tac tgc ttc      96
318 Ser Cys Asp Pro Asn Ala Phe His Ser Thr Ile Gln Leu Tyr Cys Phe
319          20          25          30
321 att tat ggc cac atc cta aat gat gtc tct gtc agc tgg cta atg gac      144
322 Ile Tyr Gly His Ile Leu Asn Asp Val Ser Val Ser Trp Leu Met Asp
323          35          40          45
325 gat cgg gag ata act gat aca ctt gca caa act gtt cta atc aag gag      192
326 Asp Arg Glu Ile Thr Asp Thr Leu Ala Gln Thr Val Leu Ile Lys Glu
327          50          55          60
329 gaa ggc aaa cta gcc tct acc tgc agt aaa ctc aac atc act gag cag      240
330 Glu Gly Lys Leu Ala Ser Thr Cys Ser Lys Leu Asn Ile Thr Glu Gln
331 65          70          75          80
333 caa tgg atg tct gaa agc acc ttc acc tgc aag gtc acc tcc caa ggc      288
334 Gln Trp Met Ser Glu Ser Thr Phe Thr Cys Lys Val Thr Ser Gln Gly
335          85          90          95
337 gta gac tat ttg gcc cac act cgg aga tgc cca gat cat gag cca cgg      336
338 Val Asp Tyr Leu Ala His Thr Arg Arg Cys Pro Asp His Glu Pro Arg
339          100          105          110
341 ggt gtg att acc tac ctg atc cca ccc agc ccc ctg gac ctg tat caa      384
342 Gly Val Ile Thr Tyr Leu Ile Pro Pro Ser Pro Leu Asp Leu Tyr Gln
343          115          120          125
345 aac ggt gct ccc aag ctt acc tgt ctg gtg gtg gac ctg gaa agc gag      432
346 Asn Gly Ala Pro Lys Leu Thr Cys Leu Val Val Asp Leu Glu Ser Glu
347          130          135          140
349 aag aat gtc aat gtg acg tgg aac caa gag aag aag act tca gtc tca      480
350 Lys Asn Val Asn Val Thr Trp Asn Gln Glu Lys Lys Thr Ser Val Ser
351 145          150          155          160
353 gca tcc cag tgg tac act aag cac cac aat aac ggc aca act agt atc      528
354 Ala Ser Gln Trp Tyr Thr Lys His His Asn Asn Gly Thr Thr Ser Ile
355          165          170          175
357 acc tcc atc ctg cct gta gtt gcc aag gac tgg att gaa ggc tac ggc      576
358 Thr Ser Ile Leu Pro Val Val Ala Lys Asp Trp Ile Glu Gly Tyr Gly
359          180          185          190
361 tat cag tgc ata gtg gac cac cct gat ttt ccc aag ccc att gtg cgt      624
362 Tyr Gln Cys Ile Val Asp His Pro Asp Phe Pro Lys Pro Ile Val Arg
363          195          200          205
365 tcc atc acc aag acc cca ggc cag cgc tca gcc ccc gag gta tat gtg      672

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 06/17/2002  
 PATENT APPLICATION: US/10/085,233A      TIME: 14:46:05

Input Set : A:\pto.vsk.txt  
 Output Set: N:\CRF3\06172002\J085233A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
 per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.  
 Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"  
 or "Unknown". Please explain source of genetic material in <220> to <223>  
 section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)  
 (Sec.1.823 of new Rules)

Seq#:2,4



## VERIFICATION SUMMARY

DATE: 06/17/2002

PATENT APPLICATION: US/10/085,233A

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Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\06172002\J085233A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:26 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1  
L:168 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:170 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:170 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:303 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:489 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:491 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:491 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: